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Proteomics and renaissance: accounts of the V Italian Proteomics Association Congress, Florence 2010

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DOI: 10.1039/c1mb90007b

In the last ten years, proteomics has been consolidating its character as a novel scientific discipline that continuously develops new questions and technologies in progressing human knowledge of complex biological systems. This worldwide movement has been guided mostly by specific local niches rather than by large consortia, as typically observed in genome projects. Such a model shares an unexpected similarity with the large number of artist workshops of the Italian Renaissance. In fact, this deeply innovative period of Italian civilization was definitely associated with masterpieces from household names (such as Michelangelo), but it was mainly a movement of humble and skilful artists whose work helped to reshape Europe. Following this model in proteomics research, local conferences represent a great opportunity to mine significant contributions of proteome science achievements. The series of themed articles published in this

issue of *Molecular BioSystems* aims to communicate to the wider scientific community the most complete and advanced studies performed by Italian Proteomics scientists.

While human proteomics investigations initially led the research in this area, the most promising applications of proteomics are presently coming from non human investigations. The advancements in this field have produced the first clinical proteomics tool (Bityper™), which is dedicated to the identification of clinical microbial isolates. The work from Lorenza Putignani and coworkers (DOI:10.1039/C0MB00138D) demonstrates how MALDI-TOF-MS pattern recognition may represent an incredibly powerful tool to obtain fast and accurate diagnosis of clinically relevant fungi, thus setting proteomics tools as potentially life-saving devices. The development of novel tools for multivariate analysis is a key issue in the technological advancement of proteomics, the paper from the group of Emilio Marengo's group (DOI:10.1039/C0MB00124D) provides a state of the art classification and ranking method for the identification of tentative biomarkers based on Principal Component Analysis and variable selection procedures. Such multivariate correlations are fundamental in order to identify relationships between molecular data and specific environmental factors, as shown in the characterization of plasma protein carbonylation in response to physical exercise in athletes presented in the study from Francesca Guidi *et al.*

(DOI:10.1039/C0MB00106F). The application of multivariate tools is also well shown in the manuscript from Laura Giusti and colleagues (DOI:10.1039/C0MB00191K) in the investigation of the parathyroid gland proteome. This study indicates the potential application of multivariate modeling in the definition of protein repertoires from adenoma and normal tissues. The multiple phenotypic correlations of the induced adaptation in a genetic model of *Salmonella enterica* is pursued in the manuscript from Domenico Ciavardelli and colleagues (DOI:10.1039/C0MB00140F) proposing a state of the art ionomics investigation by multi-elemental ICP-MS analysis coupled to parallelized quantitative shotgun LC-MS/MS for peptide profiling. This latest experimental approach has also been employed in conjunction with classical 2DE in the investigation of the platelet proteome of patients suffering the presence of a non-functional CFTR protein. The study from Luisa Pieroni and collaborators (DOI:10.1039/C0MB00135J) demonstrates *via* the construction of a functional relationships informatics network, a novel mechanism of platelet activation in patients with cystic fibrosis based on integrin signalling. A similar data-analysis approach was employed by Giovanni Nassa *et al.* (DOI:10.1039/C0MB00145G) in a comparative analysis of nuclear estrogen receptor alpha and beta interactomes in breast cancer cells and by Angelo D'Alessandro *et al.* (DOI:10.1039/C0MB00027B) with the bovine milk proteome. The protein

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adaptation to different stresses induced by aromatics is investigated by Roberto Mazzoli and colleagues in *Acinetobacter radioresistens* (DOI:10.1039/C0MB00112K) and reconstructed by ontological classification of proteins that appeared to be modulated in a wide-pI 2DE approach. The application of state of the art 2DE separation technologies is the basic experimental platform for the evaluation of quaternary structure heterogeneity of plasma apolipoprotein A1 in nephrotic syndromes in the contribution from Laura Santucci *et al.* (DOI:10.1039/C0MB00127A). This paper demonstrates the complexity of protein–protein interaction rearrangements during defined pathological conditions, casting the proteomics investigation to a new level of structural complexity. The study of the uremic biochemical milieu is also the leitmotiv of the study from Barbara Pavone and colleagues (DOI:10.1039/C0MB00137F), which identifies a long reported uremic toxin demonstrating the subtle association between structural conformational changes induced by non-enzymatic glycation of Beta2-microglobulin and the abnormal display of phosphatidylserine in human red blood cells.



It is our hope that this series of themed papers will open new opportunities for Italian proteomics scientists to collaborate with the overall international scientific community.

In the picture from right to left: Prof. Alessandra Modesti, PhD, Chairperson of the V Italian Proteomics Association Congress; Prof. Andrea Urbani, PhD, President of the Italian Proteomics Association; Dr Col. Mario Maida, M.D., Head of the Military School of Medicine Florence; Prof. Gian Franco Gensini, M.D., Head of the University of Florence School of Medicine.

Congress events

The Congress of the Italian Proteomics Association (ItPA, www.itpa.it) was held in Florence at the historical sites of the “Chiostro del Maglio” and “Chiostro Grande di Santa Maria Novella” from Wednesday 9th to Saturday 12th June, 2010. ItPA aims to

- (i) promote and support research and training in the science of Proteomics in Universities and all affiliated industries, hospitals and public research institutions

- (ii) promote and support teaching of all disciplines involved in the science of Proteomics in pre- and post-graduate University courses and in any other appropriate forum

- (iii) encourage the development of technological innovation in the science of Proteomics

- (iv) facilitate scientific communication supporting various forms of collaboration between laboratories at a national

level and the organization of congresses and meetings.

The 2010 Congress included the following five scientific sessions:

- (1) Human and Clinical Proteomics
- (2) Technological innovations and mass spectrometry
- (3) Plant Proteomics
- (4) Functional proteomics
- (5) Microbiological and Food Proteomics

Each session began with a lecture from an invited speaker. The invited speakers were:

(Opening Lecture) *Pier Paolo Pandolfi* (Boston, MA, USA) “**Pro-senescence therapy for cancer: from the enhancement of protein translation to the inhibition of protein degradation**”

Giampaolo Merlini (Pavia, Italy) “**Proteomics in pathogenesis and diagnosis of systemic amyloidoses**”

Stephen Pennington (Dublin, Ireland) “**Quantitative proteomics for biomarkers discovery and validation**”

Alex Jones (Norwich, UK) “**Phosphorylation events in plant-pathogen interactions**”

Giovanni Sindona (Cosenza, Italy) “**The Specificity of Mass Spectrometry in Biomolecular Research. Present and Future Innovation in Natural and Health Sciences**”

Maurizio Sanguinetti (Roma, Italy) “**Transition from genomics to a post-genomic era in medically relevant Fungi: application of proteomics in clinical diagnosis and biomarker discovery**”

(Closing Lecture) *Joachim Klose* (Berlin, Germany) “**Proteomics and Genomics**”